The slowly relaxing local structure approach applied to NMR relaxation in proteins

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Abstract:

We developed in recent years the slowly relaxing local structure (SRLS) approach for NMR relaxation in proteins. SRLS is a two-body (protein and probe) coupled-rotator theory where the probe executes restricted local motion. When the two rotators are timescale separated (decoupled), the main features of the standard single-body theories for treating restricted motions are recovered. The generic description consists of time correlation functions (TCFs), i.e., sums of weighted exponentials (eigenmodes), with coefficients containing the kinetic, structural and geometric information inherent in the experimental data. There is ample evidence that the theory has to allow for general tensorial properties to extract this information insightfully. This implies a multi-eigenmode scenario. We select the axiality of the local probe diffusion as an example of low tensor symmetry (typical probes are at least axially symmetric). In the presence of strong axial local ordering potentials distinct eigenmodes for the global motion, and the two components of the local motion, prevail. Weaker axial potentials mix the local motional components. When the timescale separation is not large, mode-mixing due to dynamical coupling also occurs. We assess the concerted motions as correlated or anti-correlated. It is shown that discrepancies observed recently between squared generalized order parameters from the model-free (MF) method, and a 1.2 μs long molecular dynamics (MD) trajectory, can be ascribed to oversimplified geometric features in MF. It is suggested to compare mesoscopic SRLS TCFs with their atomistic MF counterparts. One can adopt a viewpoint where the TCF comprises two (or three) eigenmodes. However, in such cases, constructs/composites act as descriptors of protein dynamics.